



SEQUENCE LISTING

<110> REGEN Biotech. Inc.

<120> The method for measuring the amount of Betaig - h 3 protein and diagnostic kit using the same

<130> 2fpo-10-14

<160> 12

<170> KopatentIn 1.71

<210> 1

<211> 683

<212> PRT

<213> Homo sapiens

<400> 1

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20 25 30

Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
35 40 45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
50 55 60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
65 70 75 80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
85 90 95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
100 105 110

Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
115 120 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
130 135 140

Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val
145 150 155 160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
 165 170 175
 Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
 180 185 190
 Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
 195 200 205
 Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala
 210 215 220
 Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr
 225 230 235 240
 Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu
 245 250 255
 Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn
 260 265 270
 Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile
 275 280 285
 Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg
 290 295 300
 Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala
 305 310 315 320
 Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu
 325 330 335
 Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile
 340 345 350
 Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp
 355 360 365
 Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala
 370 375 380
 Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu
 385 390 395 400
 Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu
 405 410 415
 Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg

420	425	430
Asn Leu Leu Arg Asn His Ile Ile	Lys Asp Gln Leu Ala Ser Lys Tyr	
435	440	445
Leu Tyr His Gly Gln Thr Leu Glu Thr	Leu Gly Gly Lys Lys Leu Arg	
450	455	460
Val Phe Val Tyr Arg Asn Ser Leu Cys Ile	Glu Asn Ser Cys Ile Ala	
465	470	475
480		
Ala His Asp Lys Arg Gly Arg Tyr Gly Thr	Leu Phe Thr Met Asp Arg	
485	490	495
Val Leu Thr Pro Pro Met Gly Thr Val Met	Asp Val Leu Lys Gly Asp	
500	505	510
Asn Arg Phe Ser Met Leu Val Ala Ala Ile	Gln Ser Ala Gly Leu Thr	
515	520	525
Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr	Val Phe Ala Pro Thr Asn	
530	535	540
Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu	Arg Ser Arg Leu Leu Gly	
545	550	555
560		
Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys	Tyr His Ile Gly Asp Glu	
565	570	575
Ile Leu Val Ser Gly Gly Ile Gly Ala Leu	Val Arg Leu Lys Ser Leu	
580	585	590
Gln Gly Asp Lys Leu Glu Val Ser Leu Lys	Asn Asn Val Val Ser Val	
595	600	605
Asn Lys Glu Pro Val Ala Glu Pro Asp Ile	Met Ala Thr Asn Gly Val	
610	615	620
Val His Val Ile Thr Asn Val Leu Gln Pro	Pro Ala Asn Arg Pro Gln	
625	630	635
640		
Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala	Leu Glu Ile Phe Lys Gln	
645	650	655
Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg	Ser Val Arg Leu Ala Pro	
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Val Tyr Gln Lys Leu Leu Glu Arg Met Lys	His	
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<210> 2
 <211> 2691
 <212> DNA
 <213> Homo sapiens

<400> 2
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 gccccaacgt gtgtgctgtg cagaagggtta ttggcactaa taggaagtac ttcaccaact 240
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 tgaaacacgg catgaccctc acctctatgt accagaattc caacatccag atccaccact 660
 atcctaattg gattgtaact gtgaactgtg cccggctcct gaaagccgac caccatgcaa 720
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cctctaagta tctgtaccat ggacagaccc tggaaactct gggcggcaaa aaactgagag	1440
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ccctggtgcg gctaaagtct ctccaagggtg acaagctgga agtcagcttg aaaaacaatg	1860
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tccttggaag aggagcttca gtattgtggg gctcataaaa catgaatcaa gcaatccagc	2460
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attataagct atgagttgaa atgttctgtc aaatgtgtct cacatctaca cgtggcttgg	2580
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<210> 3
 <211> 585
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)..(585)
 <223> 69 to 653 amino acid sequence of human ID No.1

<400> 3
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 20 25 30
 Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr
 35 40 45
 Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met
 50 55 60
 Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp
 65 70 75 80
 Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn
 85 90 95
 Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val
 100 105 110
 Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln
 115 120 125
 Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val
 130 135 140
 Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val
 145 150 155 160
 Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln
 165 170 175
 Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val
 180 185 190

Ala	Ala	Ser	Gly	Leu	Asn	Thr	Met	Leu	Glu	Gly	Asn	Gly	Gln	Tyr	Thr	195	200	205	
Leu	Leu	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Ile	Pro	Ser	Glu	Thr	210	215	220	
Leu	Asn	Arg	Ile	Leu	Gly	Asp	Pro	Glu	Ala	Leu	Arg	Asp	Leu	Leu	Asn	225	230	235	240
Asn	His	Ile	Leu	Lys	Ser	Ala	Met	Cys	Ala	Glu	Ala	Ile	Val	Ala	Gly	245	250	255	
Leu	Ser	Val	Glu	Thr	Leu	Glu	Gly	Thr	Thr	Leu	Glu	Val	Gly	Cys	Ser	260	265	270	
Gly	Asp	Met	Leu	Thr	Ile	Asn	Gly	Lys	Ala	Ile	Ile	Ser	Asn	Lys	Asp	275	280	285	
Ile	Leu	Ala	Thr	Asn	Gly	Val	Ile	His	Tyr	Ile	Asp	Glu	Leu	Leu	Ile	290	295	300	
Pro	Asp	Ser	Ala	Lys	Thr	Leu	Phe	Glu	Leu	Ala	Ala	Glu	Ser	Asp	Val	305	310	315	320
Ser	Thr	Ala	Ile	Asp	Leu	Phe	Arg	Gln	Ala	Gly	Leu	Gly	Asn	His	Leu	325	330	335	
Ser	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Leu	Ala	Pro	Leu	Asn	Ser	Val	Phe	340	345	350	
Lys	Asp	Gly	Thr	Pro	Pro	Ile	Asp	Ala	His	Thr	Arg	Asn	Leu	Leu	Arg	355	360	365	
Asn	His	Ile	Ile	Lys	Asp	Gln	Leu	Ala	Ser	Lys	Tyr	Leu	Tyr	His	Gly	370	375	380	
Gln	Thr	Leu	Glu	Thr	Leu	Gly	Gly	Lys	Lys	Leu	Arg	Val	Phe	Val	Tyr	385	390	395	400
Arg	Asn	Ser	Leu	Cys	Ile	Glu	Asn	Ser	Cys	Ile	Ala	Ala	His	Asp	Lys	405	410	415	
Arg	Gly	Arg	Tyr	Gly	Thr	Leu	Phe	Thr	Met	Asp	Arg	Val	Leu	Thr	Pro	420	425	430	
Pro	Met	Gly	Thr	Val	Met	Asp	Val	Leu	Lys	Gly	Asp	Asn	Arg	Phe	Ser	435	440	445	
Met	Leu	Val	Ala	Ala	Ile	Gln	Ser	Ala	Gly	Leu	Thr	Glu	Thr	Leu	Asn				

450		455		460
Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg				
465		470		475
				480
Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu				
	485		490	495
Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser				
	500		505	510
Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys				
	515		520	525
Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro				
	530		535	540
Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile				
	545		550	555
				560
Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln Glu Arg Gly Asp				
	565		570	575
Glu Leu Ala Asp Ser Ala Leu Glu Ile				
	580		585	

<210> 4
 <211> 1857
 <212> DNA
 <213> Mouse Intracisternal A-particle

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 accaactgca agcagtggtgta ccagaggaag atctgcggca agtcgacagt catcagttat 180
 gagtgtgtc ctggatatga aaaggtccca ggagagaaaag gttgcccagc agctcttccg 240
 ctctcaaadc tgtatgagac catgggagtt gtgggatcga ccaccacaca gctgtataca 300
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 cctagcaatg aggctgtgtc ttccttgctt gcggaagtgc tggactccct ggtgagcaac 420
 gtcaacatcg aactgctcaa tgctctccgc taccacatgg tggacaggcg ggtcctgacc 480

gatgagctca agcacggcat gaccctcacc tccatgtacc agaattccaa catccagatc 540
catcactatc ccaatgggat tgtaactggt aactgtgccc ggctgctgaa ggctgaccac 600
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aacaatgtag tgagtgtcaa taaggagcct gttgccgaaa ccgacatcat ggccacaaac 1800
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<210> 5
<211> 609

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<212>    PRT
<213>    Mouse Intracisternal A-particle

<220>
<221>    PEPTIDE
<222>    (1)..(609)
<223>    23 to 641 amino acid sequence of mouse

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 1              5              10              15

Leu Arg Gly Arg Gln His Gly Pro Asn Val Cys Ala Val Gln Lys Val
      20              25              30

Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn Cys Lys Gln Trp Tyr Gln
      35              40              45

Arg Lys Ile Cys Gly Lys Ser Thr Val Ile Ser Tyr Glu Cys Cys Pro
      50              55              60

Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly Cys Pro Ala Ala Leu Pro
      65              70              75              80

Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr Thr Thr
      85              90              95

Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met Glu Gly
      100              105              110

Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp Ala Ser
      115              120              125

Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn Ile Glu
      130              135              140

Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val Leu Thr
      145              150              155              160

Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln Asn Ser
      165              170              175

Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val Asn Cys
      180              185              190

Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val Val His
      195              200              205

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Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln Gln Ile
 210 215 220

Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val Ala Ala
 225 230 235 240

Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr Leu Leu
 245 250 255

Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr Leu Asn
 260 265 270

Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn Asn His
 275 280 285

Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly Leu Ser
 290 295 300

Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser Gly Asp
 305 310 315 320

Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp Ile Leu
 325 330 335

Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile Pro Asp
 340 345 350

Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val Ser Thr
 355 360 365

Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu Ser Gly
 370 375 380

Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe Lys Asp
 385 390 395 400

Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg Asn His
 405 410 415

Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly Gln Thr
 420 425 430

Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg Val Phe Val Tyr Arg Asn
 435 440 445

Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys Arg Gly
 450 455 460

Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro Pro Met
465 470 475 480

Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu
485 490 495

Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu
500 505 510

Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu
515 520 525

Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala
530 535 540

Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly
545 550 555 560

Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu
565 570 575

Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala
580 585 590

Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn
595 600 605

Val

<210> 6
<211> 391
<212> DNA
<213> Artificial Sequence

<220>
<223> Betaig-h3 D-IV

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catggagatc ctcaaccggg aaggggtcta cactgttttt gctcccacca atgaagcggt 180
ccaagccatg cctccagaag aactgaacaa actcttggca aatgccaagg aacttaccaa 240

catcctgaag taccacattg gtgatgaaat cctgggttagc ggaggcatcg gggccctggg 300
 gcggctgaag tctctccaag gggacaaact ggaagtcagc tcgaaaaaca atgtagtgag 360
 tgtcaataag gagcctgttg ccgaaaccga c 391

<210> 7
 <211> 140
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Betaig-h3 D-IV(1X) amino acid sequence

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 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
 20 25 30
 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
 35 40 45
 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 50 55 60
 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 65 70 75 80
 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 85 90 95
 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
 100 105 110
 Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
 115 120 125
 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn
 130 135 140

<210> 8
 <211> 280
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Betaig-h3 D-IV(2X) amino acid sequence

<400> 8

Leu	Thr	Pro	Pro	Met	Gly	Thr	Val	Met	Asp	Val	Leu	Lys	Gly	Asp	Asn
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Arg	Phe	Ser	Met	Leu	Val	Ala	Ala	Ile	Gln	Ser	Ala	Gly	Leu	Thr	Glu
		20						25				30			

Thr	Leu	Asn	Arg	Glu	Gly	Val	Tyr	Thr	Val	Phe	Ala	Pro	Thr	Asn	Glu
		35					40					45			

Ala	Phe	Arg	Ala	Leu	Pro	Pro	Arg	Glu	Arg	Ser	Arg	Leu	Leu	Gly	Asp
	50						55				60				

Ala	Lys	Glu	Leu	Ala	Asn	Ile	Leu	Lys	Tyr	His	Ile	Gly	Asp	Glu	Ile
65					70					75				80	

Leu	Val	Ser	Gly	Gly	Ile	Gly	Ala	Leu	Val	Arg	Leu	Lys	Ser	Leu	Gln
				85					90					95	

Gly	Asp	Lys	Leu	Glu	Val	Ser	Leu	Lys	Asn	Asn	Val	Val	Ser	Val	Asn
		100						105					110		

Lys	Glu	Pro	Val	Ala	Glu	Pro	Asp	Ile	Met	Ala	Thr	Asn	Gly	Val	Val
		115					120					125			

His	Val	Ile	Thr	Asn	Val	Leu	Gln	Pro	Pro	Ala	Asn	Leu	Thr	Pro	Pro
	130					135					140				

Met	Gly	Thr	Val	Met	Asp	Val	Leu	Lys	Gly	Asp	Asn	Arg	Phe	Ser	Met
145					150					155					160

Leu	Val	Ala	Ala	Ile	Gln	Ser	Ala	Gly	Leu	Thr	Glu	Thr	Leu	Asn	Arg
				165					170					175	

Glu	Gly	Val	Tyr	Thr	Val	Phe	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Arg	Ala
			180					185					190		

Leu	Pro	Pro	Arg	Glu	Arg	Ser	Arg	Leu	Leu	Gly	Asp	Ala	Lys	Glu	Leu
		195					200					205			

Ala	Asn	Ile	Leu	Lys	Tyr	His	Ile	Gly	Asp	Glu	Ile	Leu	Val	Ser	Gly
	210					215					220				

Gly	Ile	Gly	Ala	Leu	Val	Arg	Leu	Lys	Ser	Leu	Gln	Gly	Asp	Lys	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

225 230 235 240
 Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val
 245 250 255
 Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr
 260 265 270
 Asn Val Leu Gln Pro Pro Ala Asn
 275 280

<210> 9
 <211> 420
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Betaig-h3 D-IV(3X) amino acid sequence

<400> 9
 Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn
 1 5 10 15
 Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu
 20 25 30
 Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu
 35 40 45
 Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp
 50 55 60
 Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile
 65 70 75 80
 Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln
 85 90 95
 Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn
 100 105 110
 Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val
 115 120 125
 His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro
 130 135 140

Met	Gly	Thr	Val	Met	Asp	Val	Leu	Lys	Gly	Asp	Asn	Arg	Phe	Ser	Met	145	150	155	160
Leu	Val	Ala	Ala	Ile	Gln	Ser	Ala	Gly	Leu	Thr	Glu	Thr	Leu	Asn	Arg	165	170	175	
Glu	Gly	Val	Tyr	Thr	Val	Phe	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Arg	Ala	180	185	190	
Leu	Pro	Pro	Arg	Glu	Arg	Ser	Arg	Leu	Leu	Gly	Asp	Ala	Lys	Glu	Leu	195	200	205	
Ala	Asn	Ile	Leu	Lys	Tyr	His	Ile	Gly	Asp	Glu	Ile	Leu	Val	Ser	Gly	210	215	220	
Gly	Ile	Gly	Ala	Leu	Val	Arg	Leu	Lys	Ser	Leu	Gln	Gly	Asp	Lys	Leu	225	230	235	240
Glu	Val	Ser	Leu	Lys	Asn	Asn	Val	Val	Ser	Val	Asn	Lys	Glu	Pro	Val	245	250	255	
Ala	Glu	Pro	Asp	Ile	Met	Ala	Thr	Asn	Gly	Val	Val	His	Val	Ile	Thr	260	265	270	
Asn	Val	Leu	Gln	Pro	Pro	Ala	Asn	Leu	Thr	Pro	Pro	Met	Gly	Thr	Val	275	280	285	
Met	Asp	Val	Leu	Lys	Gly	Asp	Asn	Arg	Phe	Ser	Met	Leu	Val	Ala	Ala	290	295	300	
Ile	Gln	Ser	Ala	Gly	Leu	Thr	Glu	Thr	Leu	Asn	Arg	Glu	Gly	Val	Tyr	305	310	315	320
Thr	Val	Phe	Ala	Pro	Thr	Asn	Glu	Ala	Phe	Arg	Ala	Leu	Pro	Pro	Arg	325	330	335	
Glu	Arg	Ser	Arg	Leu	Leu	Gly	Asp	Ala	Lys	Glu	Leu	Ala	Asn	Ile	Leu	340	345	350	
Lys	Tyr	His	Ile	Gly	Asp	Glu	Ile	Leu	Val	Ser	Gly	Gly	Ile	Gly	Ala	355	360	365	
Leu	Val	Arg	Leu	Lys	Ser	Leu	Gln	Gly	Asp	Lys	Leu	Glu	Val	Ser	Leu	370	375	380	
Lys	Asn	Asn	Val	Val	Ser	Val	Asn	Lys	Glu	Pro	Val	Ala	Glu	Pro	Asp	385	390	395	400
Ile	Met	Ala	Thr	Asn	Gly	Val	Val	His	Val	Ile	Thr	Asn	Val	Leu	Gln				

Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala	180	185	190
Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu	195	200	205
Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly	210	215	220
Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu	225	230	235
Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val	245	250	255
Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr	260	265	270
Asn Val Leu Gln Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val	275	280	285
Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala	290	295	300
Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr	305	310	315
Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg	325	330	335
Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu	340	345	350
Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala	355	360	365
Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu	370	375	380
Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp	385	390	395
Ile Met Ala Thr Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln	405	410	415
Pro Pro Ala Asn Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu	420	425	430
Lys Gly Asp Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala			

435		440		445
Gly Leu Thr Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala				
450		455		460
Pro Thr Asn Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg				
465		470		475 480
Leu Leu Gly Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile				
	485		490	495
Gly Asp Glu Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu				
	500		505	510
Lys Ser Leu Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val				
	515		520	525
Val Ser Val Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr				
	530		535	540
Asn Gly Val Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn				
545		550		555 560

<210> 11
 <211> 5
 <212> PRT
 <213> peptide

<400> 11
 Asn Lys Asp Ile Leu
 1 5

<210> 12
 <211> 4
 <212> PRT
 <213> peptide

<400> 12
 Glu Pro Asp Ile
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